

BC  
#9



PCT09

## RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/09/674,379A

TIME: 12:19:10

Input Set : A:\ES.txt

Output Set: N:\CRF3\01292002\I674379A.raw

PS

3 &lt;110&gt; APPLICANT: Ono Pharmaceutical Co., Ltd.

5 &lt;120&gt; TITLE OF INVENTION: A novel polypeptide, a cDNA encoding the polypeptide and utilization

6 thereof

8 &lt;130&gt; FILE REFERENCE: Q61531

10 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/674,379A

11 &lt;141&gt; CURRENT FILING DATE: 2000-10-30

13 &lt;150&gt; PRIOR APPLICATION NUMBER: PCT/JP99/02284

14 &lt;151&gt; PRIOR FILING DATE: 1999-04-28

16 &lt;150&gt; PRIOR APPLICATION NUMBER: JP 10-119731

17 &lt;151&gt; PRIOR FILING DATE: 1998-04-28

19 &lt;160&gt; NUMBER OF SEQ ID NOS: 17

21 &lt;170&gt; SOFTWARE: PatentIn version 3.1

23 &lt;210&gt; SEQ ID NO: 1

24 &lt;211&gt; LENGTH: 1344

25 &lt;212&gt; TYPE: DNA

26 &lt;213&gt; ORGANISM: Mus musculus

28 &lt;400&gt; SEQUENCE: 1

ENTERED

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31 gggaatgcac agcagcagtg cacaaacggc tttgacctgg accgccagtc aggacagtgt      120
33 ctagatattg atgaatgccg gaccatccct gaggttgtgc gtggggacat gatgtgtgtc      180
35 aaccagaatg gcgggtatgt gtgcacccct cgaaccaacc cagtgtatcg agggccttac      240
37 tcaaatccct actctacatc ctactcaggc ccatacccag cagcggcccc accagtacca      300
39 gcttccaact accccacgat ttcaaggcct cttgtctgcc gctttgggta tcagatggat      360
41 gaaggcaacc agtgtgtgga tgtggacgag tgtgcaacag actcacacca gtgcaaccct      420
43 acccagatct gtatcaacac tgaaggaggt tacacctgt cctgcaccga tgggtactgg      480
45 cttctggaag ggcagtgcct agatattgat gaatgtcgt atggttactg ccagcagctc      540
47 tgtgcaaatg ttccaggatc ctattcctgt acatgcaacc ctggtttcac cctcaacgac      600
49 gatggaaggt cttgccaaga tgtgaacgag tgcgaaactg agaatccctg tgttcagacc      660
51 tgtgtcaaca cctatggctc ttatcatctgc cgctgtgacc caggatatga acttgaggaa      720
53 gatggcattc actgcagtga tatggacgag tgcagcttct ccgagttcct ctgtcaacac      780
55 gagtgtgtga accagccggg ctcatacttc tgctcgtgcc ctccaggcta cgtcctgttg      840
57 gatgataacc gaaactgcca ggatacaat gaatgtgagc accgaaacca cacgtgtacc      900
59 tcaactgcaga cttgctacaa tctacaaggg ggcttcaaat gtattgatcc catcagctgt      960
61 gaggagcctt atctgctgat tgggtgaaaac cgctgtatgt gtcctgctga gcacaccagc      1020
63 tgcagagacc agccattcac catcctgtat cgggacatgg atgtggtgtc aggacgctcc      1080
65 gttcctgctg acatcttcca gatgcaagca acaaccgat accctgggtgc ctattacatt      1140
67 ttccagatca aatctggcaa cgagggtcga gagttctata tgcggcaaac agggcctatc      1200
69 agtgccaccc tgggtgatgac acgccccatc aaagggcctc gggacatcca gctggacttg      1260
71 gagatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtgat ccgactgcgg      1320
73 atatattgtg cgcagtatcc gtcc
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76 &lt;210&gt; SEQ ID NO: 2

77 &lt;211&gt; LENGTH: 2233

78 &lt;212&gt; TYPE: DNA

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82 <221> NAME/KEY: misc_feature
83 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart
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87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (2160)..(2160)
89 <223> OTHER INFORMATION: "n" may be a, c g or t
92 <220> FEATURE:
93 <221> NAME/KEY: CDS
94 <222> LOCATION: (75)..(1418)
95 <223> OTHER INFORMATION:
98 <220> FEATURE:
99 <221> NAME/KEY: sig_peptide
100 <222> LOCATION: (75)..(143)
101 <223> OTHER INFORMATION:
104 <220> FEATURE:
105 <221> NAME/KEY: mat_peptide
106 <222> LOCATION: (144)..(1418)
107 <223> OTHER INFORMATION:
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113 cgcgcacatctt ggat atg cca gga tta aaa agg ata ctc act gtt acc atc      110
114             Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
115             -20                      -15
117 ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca      158
118 Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
119     -10             -5             -1 1             5
121 aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat      206
122 Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
123             10             15             20
125 gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc      254
126 Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
127             25             30             35
129 aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat      302
130 Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
131             40             45             50
133 cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac      350
134 Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
135     55             60             65
137 cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca      398
138 Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
139 70             75             80             85
141 agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag      446
142 Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln
143             90             95             100
145 tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct      494
146 Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro
147             105             110             115

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149	acc	cag	atc	tgt	atc	aac	act	gaa	gga	ggt	tac	acc	tgc	tcc	tgc	acc	542
150	Thr	Gln	Ile	Cys	Ile	Asn	Thr	Glu	Gly	Gly	Tyr	Thr	Cys	Ser	Cys	Thr	
151			120					125					130				
153	gat	ggg	tac	tgg	ctt	ctg	gaa	ggg	cag	tgc	cta	gat	att	gat	gaa	tgt	590
154	Asp	Gly	Tyr	Trp	Leu	Leu	Glu	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	
155		135					140						145				
157	cgc	tat	ggt	tac	tgc	cag	cag	ctc	tgt	gca	aat	gtt	cca	gga	tcc	tat	638
158	Arg	Tyr	Gly	Tyr	Cys	Gln	Gln	Leu	Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	
159	150					155					160					165	
161	tcc	tgt	aca	tgc	aac	cct	ggt	ttc	acc	ctc	aac	gac	gat	gga	agg	tct	686
162	Ser	Cys	Thr	Cys	Asn	Pro	Gly	Phe	Thr	Leu	Asn	Asp	Asp	Gly	Arg	Ser	
163					170					175					180		
165	tgc	caa	gat	gtg	aac	gag	tgc	gaa	act	gag	aat	ccc	tgt	gtt	cag	acc	734
166	Cys	Gln	Asp	Val	Asn	Glu	Cys	Glu	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	
167			185							190				195			
169	tgt	gtc	aac	acc	tat	ggc	tct	ttc	atc	tgc	cgc	tgt	gac	cca	gga	tat	782
170	Cys	Val	Asn	Thr	Tyr	Gly	Ser	Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	
171		200					205						210				
173	gaa	ctt	gag	gaa	gat	ggc	att	cac	tgc	agt	gat	atg	gac	gag	tgc	agc	830
174	Glu	Leu	Glu	Glu	Asp	Gly	Ile	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	
175		215				220					225						
177	ttc	tcc	gag	ttc	ctc	tgt	caa	cac	gag	tgt	gtg	aac	cag	ccg	ggc	tca	878
178	Phe	Ser	Glu	Phe	Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Ser	
179	230				235					240					245		
181	tac	ttc	tgc	tcg	tgc	cct	cca	ggc	tac	gtc	ctg	ttg	gat	gat	aac	cga	926
182	Tyr	Phe	Cys	Ser	Cys	Pro	Pro	Gly	Tyr	Val	Leu	Leu	Asp	Asp	Asn	Arg	
183				250					255						260		
185	agc	tgc	cag	gat	atc	aat	gaa	tgt	gag	cac	cga	aac	cac	acg	tgt	acc	974
186	Ser	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Glu	His	Arg	Asn	His	Thr	Cys	Thr	
187			265					270					275				
189	tca	ctg	cag	act	tgc	tac	aat	cta	caa	ggg	ggc	ttc	aaa	tgt	att	gat	1022
190	Ser	Leu	Gln	Thr	Cys	Tyr	Asn	Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	
191		280					285						290				
193	ccc	atc	agc	tgt	gag	gag	cct	tat	ctg	ctg	att	ggt	gaa	aac	cgc	tgt	1070
194	Pro	Ile	Ser	Cys	Glu	Glu	Pro	Tyr	Leu	Leu	Ile	Gly	Glu	Asn	Arg	Cys	
195		295				300					305						
197	atg	tgt	cct	gct	gag	cac	acc	agc	tgc	aga	gac	cag	cca	ttc	acc	atc	1118
198	Met	Cys	Pro	Ala	Glu	His	Thr	Ser	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	
199	310				315					320					325		
201	ctg	tat	cgg	gac	atg	gat	gtg	gtg	tca	gga	cgc	tcc	gtt	cct	gct	gac	1166
202	Leu	Tyr	Arg	Asp	Met	Asp	Val	Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	
203				330						335					340		
205	atc	ttc	cag	atg	caa	gca	aca	acc	cga	tac	cct	ggt	gcc	tat	tac	att	1214
206	Ile	Phe	Gln	Met	Gln	Ala	Thr	Thr	Arg	Tyr	Pro	Gly	Ala	Tyr	Tyr	Ile	
207			345						350				355				
209	ttc	cag	atc	aaa	tct	ggc	aac	gag	ggt	cga	gag	ttc	tat	atg	cgg	caa	1262
210	Phe	Gln	Ile	Lys	Ser	Gly	Asn	Glu	Gly	Arg	Glu	Phe	Tyr	Met	Arg	Gln	
211			360				365						370				
213	aca	ggg	cct	atc	agt	gcc	acc	ctg	gtg	atg	aca	cgc	ccc	atc	aaa	ggg	1310

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214 Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly  
 215 375 380 385  
 217 cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc 1358  
 218 Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val  
 219 390 395 400 405  
 221 atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tgc 1406  
 222 Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser  
 223 410 415 420  
 225 cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag 1458  
 226 Gln Tyr Pro Phe  
 227 425  
 229 caccgagggg cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac 1518  
 231 ctttcctgct gaatatctcc tggggggcatc agcctagcat cttgacccat atctgtacta 1578  
 233 ttgcagatgg tcaactctgaa ggacaccctg ccctcagttc ctatgatgca gttatccaaa 1638  
 235 agtgttcatc ttagcccctg atatgagggt gccagtgaact cttcaaagcc ttccatttat 1698  
 237 ttccatcggt ttataaaaaa gaaaatagat tagatttgcg ggggtatgag tcctcgaagg 1758  
 239 ttcaaagac tgagtggctt gctctcacct ctctctctcc ttctctccatc tcttgctgca 1818  
 241 ttgctgcttt gcaaaagtc tcatgggctc gtgggaaatg ctgggaatag ctagtgttgc 1878  
 243 tcttgcatgt tctgagaagg ctatgggaac acaccacagc aggatcgaag gtttttatag 1938  
 245 agtctatttt aaaatcacat ctgggtatttt cagcataaaa gaaatttttag ttgtctttaa 1998  
 247 aatttgtag agtggttaac cttttcttat tcattttgag gcttctttaa gtggtagaat 2058  
 249 tccttccaaa ggcctcagat acatgttatg ttcagttctt ccaacctcat cctttcctgc 2118  
 251 atcttagccc agttttttacg aagacccctt aatcatgctt tnttaagagt ttttacccaa 2178  
 253 ctgcgttga agacagaggt atccagactg attaaataat tgaagaaaaa aaaaa 2233  
 256 <210> SEQ ID NO: 3  
 257 <211> LENGTH: 448  
 258 <212> TYPE: PRT  
 259 <213> ORGANISM: Mus musculus  
 261 <220> FEATURE:  
 262 <221> NAME/KEY: misc\_feature  
 263 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart  
 266 <400> SEQUENCE: 3  
 268 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Trp  
 269 -20 -15 -10  
 272 Leu Pro His Pro Gly Asn Ala Gln Gln Cys Thr Asn Gly Phe Asp  
 273 -5 -1 1 5  
 276 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr  
 277 10 15 20 25  
 280 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly  
 281 30 35 40  
 284 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr  
 285 45 50 55  
 288 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala  
 289 60 65 70  
 292 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val  
 293 75 80 85  
 296 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val  
 297 90 95 100 105  
 300 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys

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301          110          115          120
304 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
305          125          130          135
308 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
309          140          145          150
312 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
313          155          160          165
316 Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val
317 170          175          180          185
320 Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
321          190          195          200
324 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
325          205          210          215
328 Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
329          220          225          230
332 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser
333          235          240          245
336 Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
337 250          255          260          265
340 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr
341          270          275          280
344 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys
345          285          290          295
348 Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala
349          300          305          310
352 Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
353          315          320          325
356 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
357 330          335          340          345
360 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
361          350          355          360
364 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
365          365          370          375
368 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
369          380          385          390
372 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
373          395          400          405
376 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
377 410          415          420          425
380 <210> SEQ ID NO: 4
381 <211> LENGTH: 423
382 <212> TYPE: PRT
383 <213> ORGANISM: Mus musculus
385 <220> FEATURE:
386 <221> NAME/KEY: MISC_FEATURE
387 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart
390 <400> SEQUENCE: 4
392 Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
393 1          5          10          15

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→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,379A

DATE: 01/29/2002

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Input Set: A:\ES.txt

Output Set: N:\CRF3\01292002\I674379A.raw

L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16